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O 10 < IntelliGenetics:  
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FastDB<sup>N</sup>- Fast Pairwise Comparison of Sequences  
Release 5.4

Results file us-09-125-005-6.res made by sdavid on Thu 2 Aug 101 10:06:27-PST.  
Query sequence being compared:US-09-125-005-6 (1-636)  
Number of sequences searched: 2  
Number of scores above cutoff: 2

Results of the initial comparison of US-09-125-005-6 (1-636), with:

File : PCTUS9914057.pep

100-

-

50-

-

M-

B-

E-

U-

E-

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1. PCT-US99-14057-1 Sequence 1, Application P 636 636 636 0.71 0

The list of other best scores is:

Sequence Name Description Length Score Score Sig. Frame

2. PCT-US99-14057-2 Sequence 2, Application P 499 492 494 -0.71 0

1. US-09-125-005-6 (1-636)  
PCT-US99-14057-1 Sequence 1, Application PC/TUS9914057

Sequence 1, Application PC/TUS9914057

GENERAL INFORMATION:  
APPLICANT: El-Deliry, Wafik  
TITLE OF INVENTION: Compositions and Methods for Inducing Apoptosis in E6-Expressing Cells

FILE REFERENCE: Penn K-1824  
CURRENT APPLICATION NUMBER: PCT/US99/14057  
CURRENT FILING DATE: 1999-06-23

EARLIER APPLICATION NUMBER: 60/090,526  
EARLIER FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 3  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO: 1  
LENGTH: 636

TYPE: PRT  
ORGANISM: Homo sapiens

PUBLICATION INFORMATION:  
AUTHORS: Kaghad, M.; Bonnet, H.; Yang, A.; Creanchter, L.; B

JOURNAL: Monocleically expressed gene related to p53 at 1  
VOLUME: 90  
ISSUE: 4  
PAGES: 809-819  
DATE: 1997-08-22

DATABASE ACCESSION NUMBER: Genbank Y11416  
DATABASE ENTRY DATE: 1997-09-02

Initial Score = 636 Optimized Score = 636 Significance = 0.71  
Residue Identity = 100% Matches = 636 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60 70  
MAQSPATSPGGTPEHLSSLEPDSTYDLQSSRGNNNEVGGTDSMDVFLLEGMTSYMAQFNLLSTM  
X 11 21 31 41 51 61 71 81  
MAQSPATSPGGTPEHLSSLEPDSTYDLQSSRGNNNEVGGTDSMDVFLLEGMTSYMAQFNLLSTM  
X 12 22 32 42 52 62 72 82  
MAQSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 13 23 33 43 53 63 73 83  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 14 24 34 44 54 64 74 84  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 15 25 35 45 55 65 75 85  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 16 26 36 46 56 66 76 86  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 17 27 37 47 57 67 77 87  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 18 28 38 48 58 68 78 88  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 19 29 39 49 59 69 79 89  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 20 30 40 50 60 70 80 90  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 21 31 41 51 61 71 81 91  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 22 33 43 53 63 73 83 93  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 23 34 44 54 64 74 84 94  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 24 35 45 55 65 75 85 95  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 25 36 46 56 66 76 86 96  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 26 37 47 57 67 77 87 97  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 27 38 48 58 68 78 88 98  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 28 39 49 59 69 79 89 99  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 29 40 50 60 70 80 90 100  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 30 41 51 61 71 81 91 101  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 31 42 52 62 72 82 92 102  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 32 43 53 63 73 83 93 103  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 33 44 54 64 74 84 94 104  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 34 45 55 65 75 85 95 105  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 35 46 56 66 76 86 96 106  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 36 47 57 67 77 87 97 107  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 37 48 58 68 78 88 98 108  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 38 49 59 69 79 89 99 109  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 39 50 60 70 80 90 100 110  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 40 51 61 71 81 91 101 111  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 41 52 62 72 82 92 102 112  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 42 53 63 73 83 93 103 113  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 43 54 64 74 84 94 104 114  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 44 55 65 75 85 95 105 115  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 45 56 66 76 86 96 106 116  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 46 57 67 77 87 97 107 117  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 47 58 68 78 88 98 108 118  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 48 59 69 79 89 99 109 119  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 49 60 70 80 90 100 110 120  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 50 61 71 81 91 101 111 121  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 51 62 72 82 92 102 112 122  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 52 63 73 83 93 103 113 123  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 53 64 74 84 94 104 114 124  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 54 65 75 85 95 105 115 125  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 55 66 76 86 96 106 116 126  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 56 67 77 87 97 107 117 127  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 57 68 78 88 98 108 118 128  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 58 69 79 89 99 109 119 129  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 59 70 80 90 100 110 120 130  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 60 71 81 91 101 111 121 131  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 61 72 82 92 102 112 122 132  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 62 73 83 93 103 113 123 133  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 63 74 84 94 104 114 124 134  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 64 75 85 95 105 115 125 135  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 65 76 86 96 106 116 126 136  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 66 77 87 97 107 117 127 137  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 67 78 88 98 108 118 128 138  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 68 79 89 99 109 119 129 139  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 69 80 90 100 110 120 130 140  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 70 81 91 101 111 121 131 141  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 71 82 92 102 112 122 132 142  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 72 83 93 103 113 123 133 143  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 73 84 94 104 114 124 134 144  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 74 85 95 105 115 125 135 145  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 75 86 96 106 116 126 136 146  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 76 87 97 107 117 127 137 147  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 77 88 98 108 118 128 138 148  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 78 89 99 109 119 129 139 149  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 79 90 100 110 120 130 140 150  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 80 91 101 111 121 131 141 151  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 81 92 102 112 122 132 142 152  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 82 93 103 113 123 133 143 153  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 83 94 104 114 124 134 144 154  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 84 95 105 115 125 135 145 155  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 85 96 106 116 126 136 146 156  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 86 97 107 117 127 137 147 157  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 87 98 108 118 128 138 148 158  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 88 99 109 119 129 139 149 159  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 89 100 110 120 130 140 150 160  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 90 101 111 121 131 141 151 161  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 91 102 112 122 132 142 152 162  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 92 103 113 123 133 143 153 163  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 93 104 114 124 134 144 154 164  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 94 105 115 125 135 145 155 165  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 95 106 116 126 136 146 156 166  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 96 107 117 127 137 147 157 167  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 97 108 118 128 138 148 158 168  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 98 109 119 129 139 149 159 169  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 99 110 120 130 140 150 160 170  
DQMSSRAASASSPYPTPEHALSSVPTSPYACPSSTFDTMSPAPVTPSNTDYPGPSPHFEVTFQQSSTASATWY  
X 100 10:00:00.00 00:00:00.00

Number of residues:

Number of sequences searched:

Number of scores above cutoff:

The scores below are sorted by initial score.

Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found.

Sequence Name Description Length Score Score Sig. Frame

US-09-125-005-6 (1-636)  
PCT-US99-14057-2 Sequence 2, Application PC/TUS9914057

Sequence 2, Application PC/TU9914057  
GENERAL INFORMATION:  
APPLICANT: EL-DEIRY, Wafik  
TITLE OF INVENTION: Compositions and Methods for Inducing Apoptosis in E6-Expressing Cells  
REFERENCE: Penn K-1824  
CURRENT APPLICATION NUMBER: PCT/US99/14057  
CURRENT FILING DATE: 1999-06-13  
EARLIER APPLICATION NUMBER: 60/090,526  
EARLIER FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: FastSEQ for Windows Version 3.0

Q\_ID NO 2  
LENGTH: 499  
TYPE: PRT  
ORGANISM: *Homo sapiens*  
PUBLICATION INFORMATION:  
AUTHORS: Kagnad et al.  
TITLE: Monoallelically expressed gene related to p53 at 1

VOLUME: 90  
ISSUE: 4  
PAGES: 809-819  
DATE: 1997-08-22  
DATABASE ACCESSION NUMBER: Genbank Y11416

Initial Score	492	Optimized Score	.494	Significance	-0.71
Initial Identity	98%	Matched	.494	Mismatches	5
s	0	Conservative Substitutions			0

X	MAQSTATSPDGTTTFFHLWSSLEPDSTYFDLPOSQRGNNEVYGGTDSMDYFHLEGMTSYMAQFNLSSSTM	10	20	30	40	50	60	70
X	MAQSTATSPDGTTTFFHLWSSLEPDSTYFDLPOSQRGNNEVYGGTDSMDYFHLEGMTSYMAQFNLSSSTM	10	20	30	40	50	60	70
X	DOMSRSASASPTPHEAASVPTHSPYAQPSSTFDMSPAVIPNTDYGPHHFTEVFOQSSTPKSATWY	80	90	100	110	120	130	140
X	DOMSRSASASPTPHEAASVPTHSPYAQPSSTFDMSPAVIPNTDYGPHHFTEVFOQSSTPKSATWY	80	90	100	110	120	130	140
X	DOMSRSASASPTPHEAASVPTHSPYAQPSSTFDMSPAVIPNTDYGPHHFTEVFOQSSTPKSATWY	80	90	100	110	120	130	140

· SPLLKLYCQIAKTCPIQKVSTPPPPGTAIRAMPVYKKAEEHTDVKRCPNHELGDFNEGOSAPASHLIR · 150 160 170 180 190 200 210

||||||| SPILKKLYCQIATKPTQIKVSTPPIPQVYKRAEHTDVKRCPNELGRDFNECOSAPASHLIR  
 ||||||| 150 160 170 180 190 200 210  
 ||||||| 220 230 240 250 260 270 280  
 VGGNNLQQYDVPPYTGROSUVYPPQVGTETTILYLNFMCISSCGMMNRPILLITLEMRDQVLGRR  
 ||||||| 220 230 240 250 260 270 280  
 VGGNNLQQYDVPPYTGROSUVYPPQVGTETTILYLNFMCISSCGMMNRPILLITLEMRDQVLGRR  
 ||||||| 220 230 240 250 260 270 280  
 SEGRICACPRDKADEDFYEQDNLNESSAKNGAASRKFQSPVPAAGYVKKRHDDEDTYLQVR  
 ||||||| 220 230 240 250 260 270 280  
 SEGRICACPRDKADEDFYEQDNLNESSAKNGAASRKFQSPVPAAGYVKKRHDDEDTYLQVR  
 ||||||| 220 230 240 250 260 270 280  
 GRENFEILMLKLESELMLMELVPPQPLDSDTROOQDOLLORESHQOPPSGPVLSQPMNKVHGGMNKLPSVNWLVG  
 ||||||| 220 230 240 250 260 270 280  
 GRENFEILMLKLESELMLMELVPPQPLDSDTROOQDOLLORESHQOPPSGPVLSQPMNKVHGGMNKLPSVNWLVG  
 ||||||| 220 230 240 250 260 270 280  
 QPPPHSSAATPNLGPVGPGLNNGHAYPANGEMSSSISAOSMVGSSICTPPPYHADPSLVSLEJLGCPN  
 ||||||| 220 230 240 250 260 270 280  
 QPPPHSSAATPNLGPVGPGLNNGHAYPANGEMSSSISAQSVHSQVSGSSICTPPPYHADPSLVRWTGP  
 ||||||| 220 230 240 250 260 270 280  
 440 450 460 470 480 490 500  
 QPPPHSSAATPNLGPVGPGLNNGHAYPANGEMSSSISAOSMVGSSICTPPPYHADPSLVSLEJLGCPN  
 ||||||| 220 230 240 250 260 270 280  
 QPPPHSSAATPNLGPVGPGLNNGHAYPANGEMSSSISAQSVHSQVSGSSICTPPPYHADPSLVRWTGP  
 ||||||| 220 230 240 250 260 270 280  
 440 450 460 470 480 490 X